```
SEQ ID 2    1 ATG TTG CAG ATG GCT GGG CAG TGC TCC CAA AAT GAA TAT TTT GAC AGT TTG TTG CAT GCT
SEQ ID 1    1▸ M   L   Q   M   A   G   Q   C   S   Q   N   E   Y   F   D   S   L   L   H   A
           61 TGC ATA CCT TGT CAA CTT CGA TGT TCT TCT AAT ACT CCT CCT CTA ACA TGT CAG CGT TAT
           21▸ C   I   P   C   Q   L   R   C   S   S   N   T   P   P   L   T   C   Q   R   Y
          121 TGT AAT GCA AGT GTG ACC AAT TCA GTG AAA GGA ACG AAT GCG ATT CTC TGG ACC TGT TTG
           41▸ C   N   A   S   V   T   N   S   V   K   G   T   N   A   I   L   W   T   C   L
          181 GGA CTG AGC TTA ATA ATT TCT TTG GCA GTT TTC GTG CTA ATG TTT TTG CTA AGG AAG ATA
           61▸ G   L   S   L   I   I   S   L   A   V   F   V   L   M   F   L   L   R   K   I
          241 AGC TCT GAA CCA TTA AAG GAC GAG TTT AAA AAC ACA GGA TCA GGT CTC CTG GGC ATG GCT
           81▸ S   S   E   P   L   K   D   E   F   K   N   T   G   S   G   L   L   G   M   A
          301 AAC ATT GAC CTG GAA AAG AGC AGG ACT GGT GAT GAA ATT ATT CTT CCG AGA GGC CTC GAG
          101▸ N   I   D   L   E   K   S   R   T   G   D   E   I   I   L   P   R   G   L   E
          361 TAC ACG GTG GAA GAA TGC ACC TGT GAA GAC TGC ATC AAG AGC AAA CCG AAG GTC GAC TCT
          121▸ Y   T   V   E   E   C   T   C   E   D   C   I   K   S   K   P   K   V   D   S
          421 GAC CAT TGC TTT CCA CTC CCA GCT ATG GAG GAA GGC GCA ACC ATT CTT GTC ACC ACG AAA
          141▸ D   H   C   F   P   L   P   A   M   E   E   G   A   T   I   L   V   T   T   K
          481 ACG AAT GAC TAT TGC AAG AGC CTG CCA GCT GCT TTG AGT GCT ACG GAG ATA GAG AAA TCA
          161▸ T   N   D   Y   C   K   S   L   P   A   A   L   S   A   T   E   I   E   K   S
          541 ATT TCT GCT AGG TAA
          181▸ I   S   A   R   •
```

FIG. 1

FIG. 2A

FIG. 2B

FIG. 2

```
             1  ATG GAG ACA GAC ACA CTC CTG TTA TGG GTG CTG CTG CTC TGG GTT CCA GGT TCC ACT GGT
             1▸
SEQ ID 4     1▸  M   E   T   D   T   L   L   L   W   V   L   L   L   W   V   P   G   S   T   G
SEQ ID 3    61  GAC GTC ACG ATG TTG CAG ATG GCT GGG CAG TGC TCC CAA AAT GAA TAT TTT GAC AGT TTG
                            1▸ M   L   Q   M   A   G   Q   C   S   Q   N   E   Y   F   D   S   L
            21▸  D   V   T   M   L   Q   M   A   G   Q   C   S   Q   N   E   Y   F   D   S   L
           121  TTG CAT GCT TGC ATA CCT TGT CAA CTT CGA TGT TCT TCT AAT ACT CCT CCT CTA ACA TGT
            18▸  L   H   A   C   I   P   C   Q   L   R   C   S   S   N   T   P   P   L   T   C
            41▸  L   H   A   C   I   P   C   Q   L   R   C   S   S   N   T   P   P   L   T   C
           181  CAG CGT TAT TGT AAT GCA AGT GTG ACC AAT TCA GTG AAA GGA GTC GAC AAA ACT CAC ACA
            38▸  Q   R   Y   C   N   A   S   V   T   N   S   V   K   G
            61▸  Q   R   Y   C   N   A   S   V   T   N   S   V   K   G   V   D   K   T   H   T
           241  TGC CCA CCG TGC CCA GCA CCT GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA

            81▸  C   P   P   C   P   A   P   E   L   L   G   G   P   S   V   F   L   F   P   P
           301  AAA CCC AAG GAC ACC CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC

           101▸  K   P   K   D   T   L   M   I   S   R   T   P   E   V   T   C   V   V   V   D
           361  GTG AGC CAC GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT

           121▸  V   S   H   E   D   P   E   V   K   F   N   W   Y   V   D   G   V   E   V   H
           421  AAT GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC GTC

           141▸  N   A   K   T   K   P   R   E   E   Q   Y   N   S   T   Y   R   V   V   S   V
           481  CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC
```

FIG. 2A

```
161▸ L   T   V   L   H   Q   D   W   L   N   G   K   E   Y   K   C   K   V   S   N
541  AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA GGG CAG CCC CGA GAA

181▸ K   A   L   P   A   P   I   E   K   T   I   S   K   A   K   G   Q   P   R   E
601  CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG ACC AAG AAC CAG GTC AGC CTG

201▸ P   Q   V   Y   T   L   P   P   S   R   D   E   L   T   K   N   Q   V   S   L
661  ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC ATC GCC GTG GAG TGG GAG AGC AAT GGG

221▸ T   C   L   V   K   G   F   Y   P   S   D   I   A   V   E   W   E   S   N   G
721  CAG CCG GAG AAC AAC TAC AAG ACC ACG CCT CCC GTG TTG GAC TCC GAC GGC TCC TTC TTC

241▸ Q   P   E   N   N   Y   K   T   T   P   P   V   L   D   S   D   G   S   F   F
781  CTC TAC AGC AAG CTC ACC GTG GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC

261▸ L   Y   S   K   L   T   V   D   K   S   R   W   Q   Q   G   N   V   F   S   C
841  TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCC

281▸ S   V   M   H   E   A   L   H   N   H   Y   T   Q   K   S   L   S   L   S   P
901  GGG AAA TGA

301▸ G   K   •
```

FIG. 2B

```
                                                            BsaAI        BbsI
  1 AAGACTCAAA CTTAGAAACT TGAATTAGAT GTGGTATTCA AATCCTTACG TGCCGCGAAG
 61 ACACAGACAG CCCCCGTAAG AACCCACGAA GCAGGCGAAG TTCATTGTTC TCAACATTCT
                              EcoRI
121 AGCTGCTCTT GCTGCATTTG CTCTGGAATT CTTGTAGAGA TATTACTTGT CCTTCCAGGC
          SfcI                         BclI
181 TGTTCTTTCT GTAGCTCCCT TGTTTTCTTT TTGTGATCAT GTTGCAGATG GCTGGGCAGT
                                         1▶ M  L  Q  M  A  G  Q
                 SspI                    SphI            HincII
241 GCTCCCAAAA TGAATATTTT GACAGTTTGT TGCATGCTTG CATACCTTGT CAACTTCGAT
  8▶C  S  Q  N  E  Y  F  D  S  L  L  H  A  C  I  P  C  Q  L  R
                              Pci I
                              AflIII
301 GTTCTTCTAA TACTCCTCCT CTAACATGTC AGCGTTATTG TAATGCAAGT GTGACCAATT
 28▶C  S  S  N  T  P  P  L  T  C  Q  R  Y  C  N  A  S  V  T  N
                                             BsmFI
361 CAGTGAAAGG AACGAATGCG ATTCTCTGGA CCTGTTTGGG ACTGAGCTTA ATAATTTCTT
 48▶S  V  K  G  T  N  A  I  L  W  T  C  L  G  L  S  L  I  I  S
421 TGGCAGTTTT CGTGCTAATG TTTTTGCTAA GGAAGATAAG CTCTGAACCA TTAAAGGACG
 68▶L  A  V  F  V  L  M  F  L  L  R  K  I  S  S  E  P  L  K  D
       DraI          AlwI      BsaI
481 AGTTTAAAAA CACAGGATCA GGTCTCCTGG GCATGGCTAA CATTGACCTG GAAAAGAGCA
 88▶E  F  K  N  T  G  S  G  L  L  G  M  A  N  I  D  L  E  K  S
                XmnI                  StuI  XhoI
541 GGACTGGTGA TGAAATTATT CTTCCGAGAG GCCTCGAGTA CACGGTGGAA GAATGCACCT
108▶R  T  G  D  E  I  I  L  P  R  G  L  E  Y  T  V  E  E  C  T
                                    SalI
                                    HincII
       BbsI                         AccI
601 GTGAAGACTG CATCAAGAGC AAACCGAAGG TCGACTCTGA CCATTGCTTT CCACTCCCAG
128▶C  E  D  C  I  K  S  K  P  K  V  D  S  D  H  C  F  P  L  P
661 CTATGGAGGA AGGCGCAACC ATTCTTGTCA CCACGAAAAC GAATGACTAT TGCAAGAGCC
148▶A  M  E  E  G  A  T  I  L  V  T  T  K  T  N  D  Y  C  K  S
       PvuII
721 TGCCAGCTGC TTTGAGTGCT ACGGAGATAG AGAAATCAAT TTCTGCTAGG TAATTAACCA
168▶L  P  A  A  L  S  A  T  E  I  E  K  S  I  S  A  R
          XhoI            DraI                                BglII
781 TTTCGACTCG AGCAGTGCCA CTTTAAAAAT CTTTTGTCAG AATAGATGAT GTGTCAGATC
841 TCTTTAGGAT GACTGTATTT TTCAGTTGCC GATACAGCTT TTTGTCCTCT AACTGTGGAA
                                                                  StyI
901 ACTCTTTATG TTAGATATAT TTCTCTAGGT TACTGTTGGG AGCTTAATGG TAGAAACTTC
961 CTTGGTTTCA TGATTAAAGT CTTTTTTTTT CCTGA
```

FIG. 3

SRUCTURE COMPARISON BETWEEN TNF-R55 AND BAFF-R

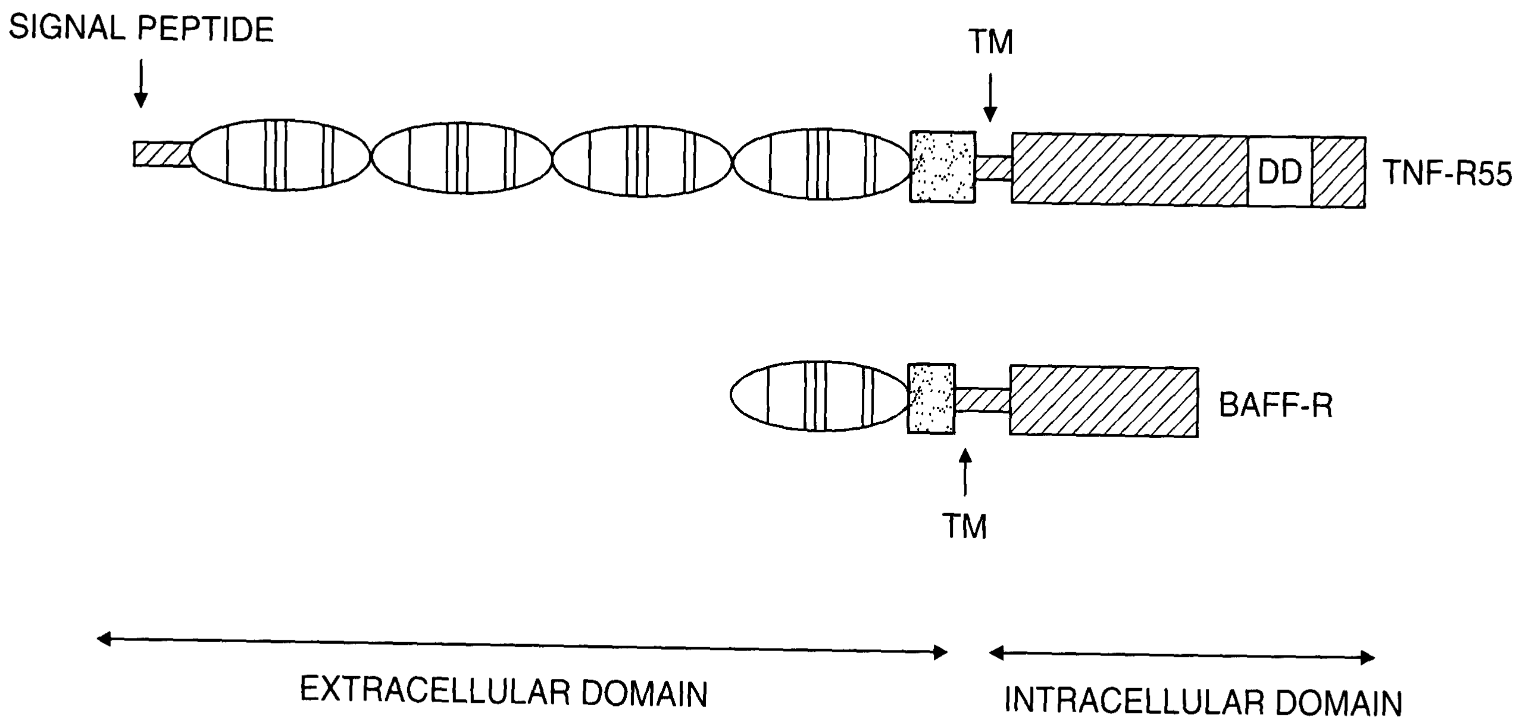


FIG. 4

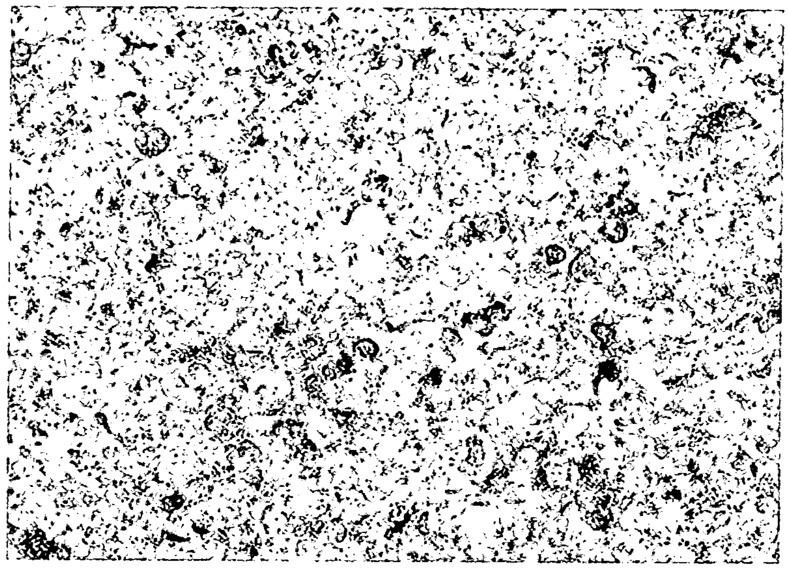


FIG. 5A

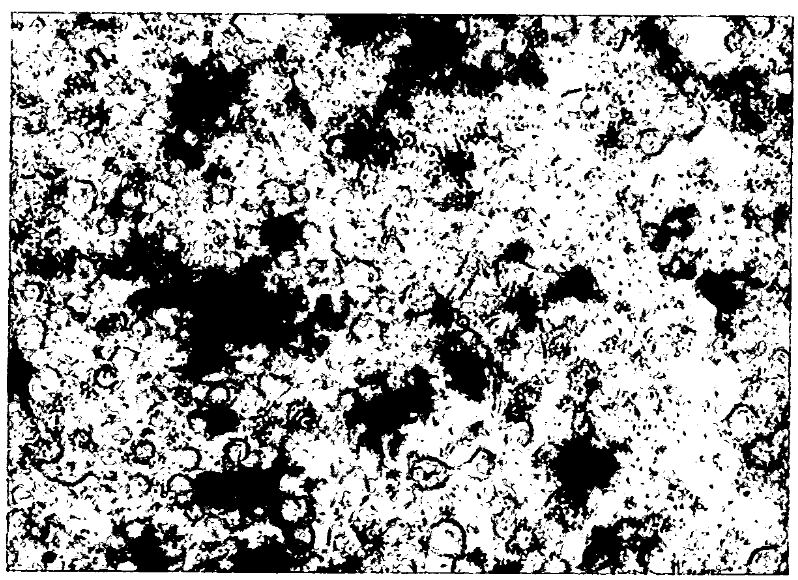


FIG. 5B

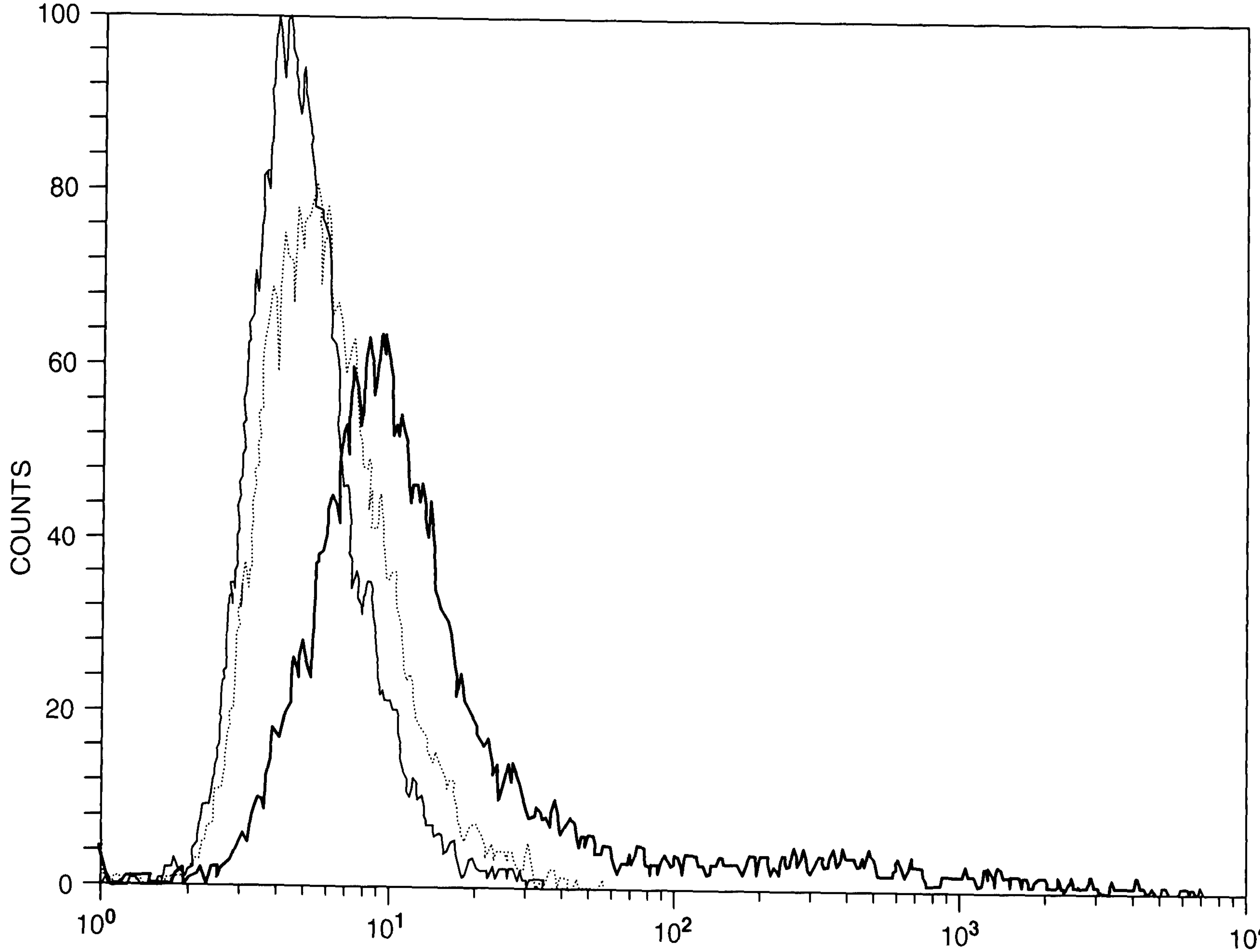
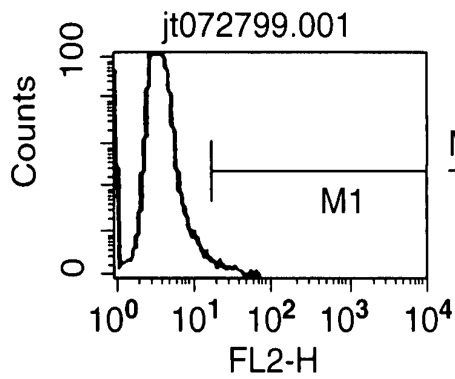
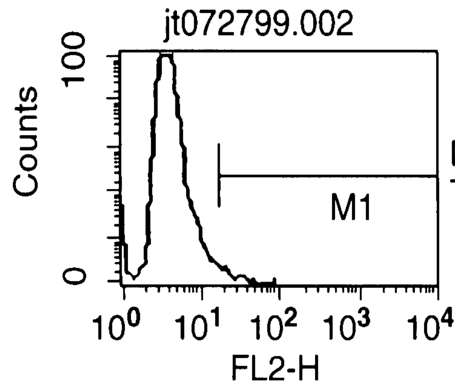


FIG. 6A



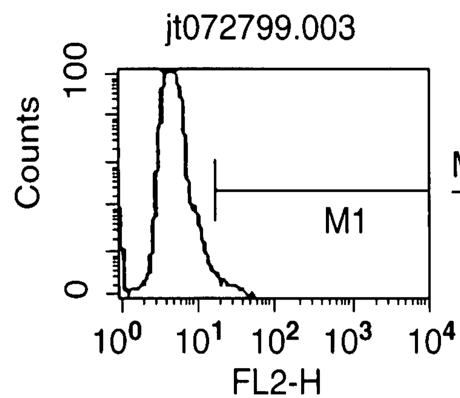
Marker	Left	Right	Events	% Gated	% Total	Mean	Geo Mean	CV	Median
All	1.	9910	10000	100.00	100.00	4.26	3.80	61.34	3.65
M1	17.	9910	65	0.65	0.65	23.23	22.44	30.37	20.35

FIG. 6B-1



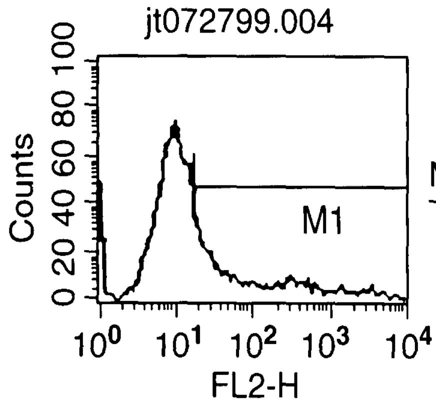
Marker	Left	Right	Events	% Gated	% Total	Mean	Geo Mean	CV	Median
All	1.	9910	10000	100.00	100.00	4.61	4.11	61.98	3.89
M1	17.	9910	79	0.79	0.79	22.88	21.98	34.94	19.63

FIG. 6B-2



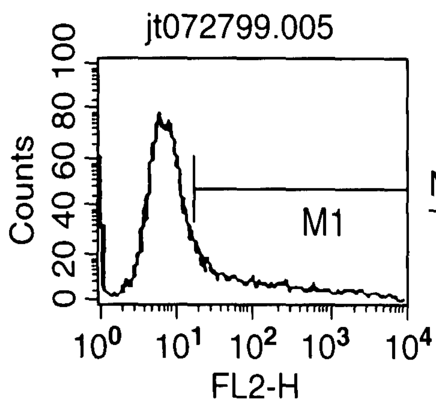
Marker	Left	Right	Events	% Gated	% Total	Mean	Geo Mean	CV	Median
All	1.	9910	10000	100.00	100.00	5.51	4.93	58.41	4.66
M1	17.	9910	130	1.30	1.30	23.55	22.98	23.39	22.57

FIG. 6B-3



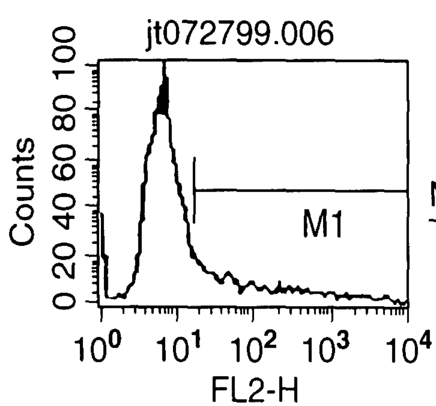
Marker	Left	Right	Events	% Gated	% Total	Mean	Geo Mean	CV	Median
All	1.	9910	10000	100.00	100.00	108.24	15.40	459.27	10.27
M1	17.	9910	2785	27.85	27.85	366.10	85.21	243.61	45.32

FIG. 6B-4



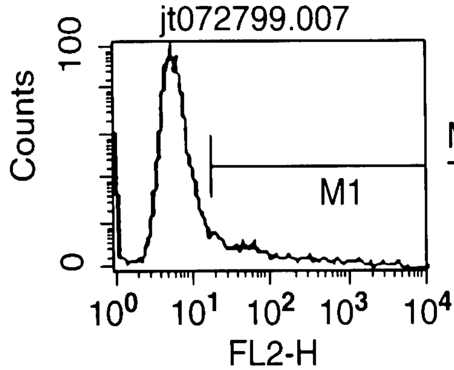
Marker	Left	Right	Events	% Gated	% Total	Mean	Geo Mean	CV	Median
All	1.	9910	10000	100.00	100.00	72.53	11.42	516.47	7.84
M1	17.	9910	2054	20.54	20.54	324.52	88.86	239.37	61.80

FIG. 6B-5



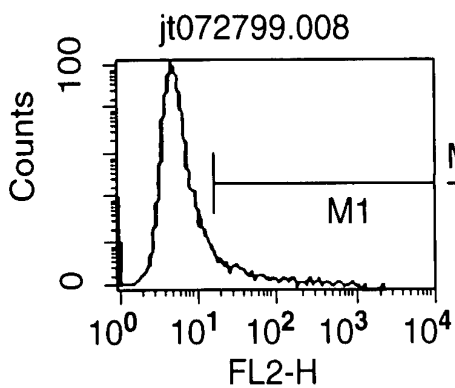
Marker	Left	Right	Events	% Gated	% Total	Mean	Geo Mean	CV	Median
All	1.	9910	10000	100.00	100.00	51.15	9.41	566.98	6.67
M1	17.	9910	1673	16.73	16.73	272.40	81.97	244.63	54.25

FIG. 6B-6



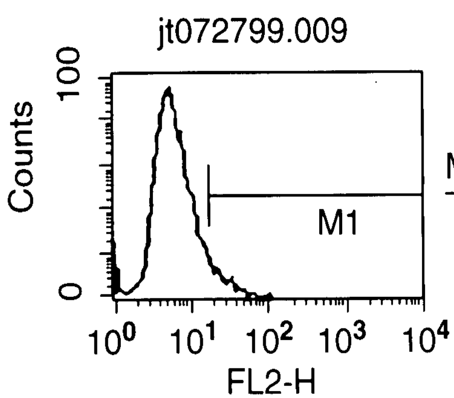
Marker	Left	Right	Events	% Gated	% Total	Mean	Geo Mean	CV	Median
All	1.	9910	10000	100.00	100.00	26.59	7.74	576.94	5.94
M1	17.	9910	1313	13.13	13.13	161.35	60.77	246.67	42.94

FIG. 6B-7



Marker	Left	Right	Events	% Gated	% Total	Mean	Geo Mean	CV	Median
All	1.	9910	10000	100.00	100.00	12.39	6.54	405.32	5.47
M1	17.	9910	876	8.76	8.76	78.94	43.41	195.84	33.68

FIG. 6B-8



Marker	Left	Right	Events	% Gated	% Total	Mean	Geo Mean	CV	Median
All	1.	9910	10000	100.00	100.00	6.99	6.60	69.06	5.67
M1	17.	9910	393	3.93	3.93	24.33	23.31	33.78	21.48

FIG. 6B-9

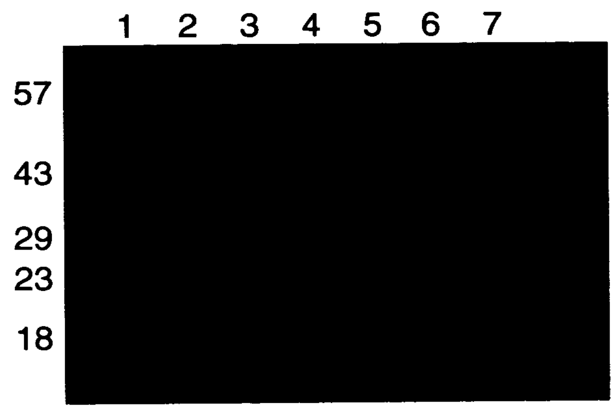

1
2
3
4
5
6
7
57
43
29
23
18

FIG. 7

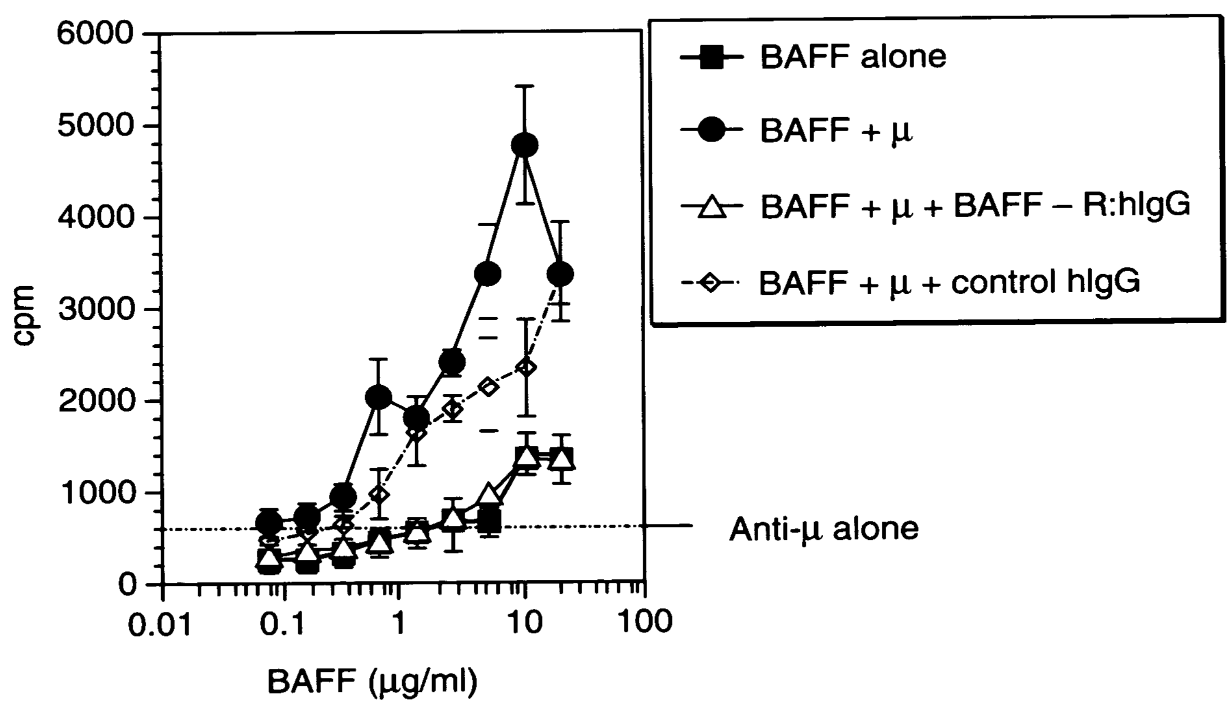
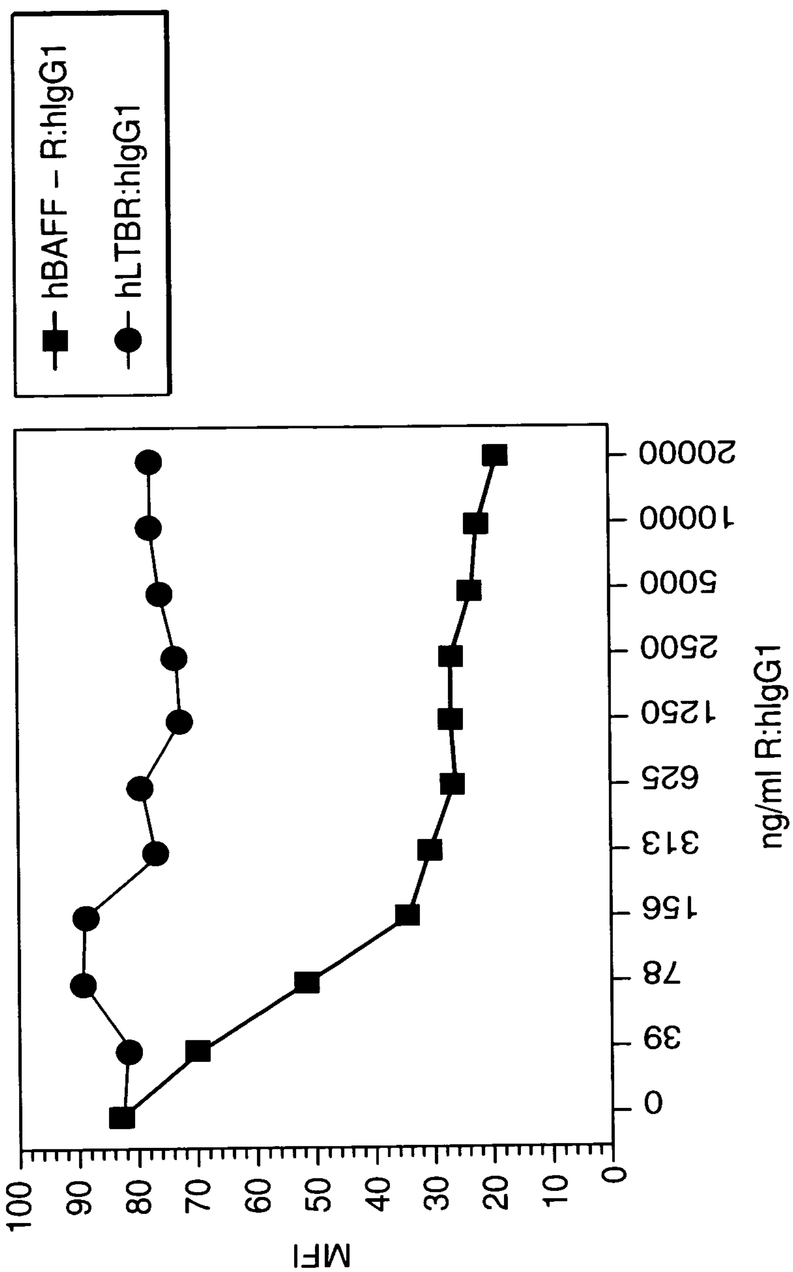

6000
5000
4000
3000
2000
1000
0
cpm
0.01
0.1
1
10
100
BAFF (μg/ml)
BAFF alone
BAFF + μ
BAFF + μ + BAFF – R:hIgG
BAFF + μ + control hIgG
Anti-μ alone

FIG. 8



hBAFF – R:hIgG1
hLTBR:hIgG1
MFI
100
90
80
70
60
50
40
30
20
10
0
0
39
78
156
313
625
1250
2500
5000
10000
20000
ng/ml R:hIgG1

FIG. 9

FIG. 10A

BCMA-Ig Treatment Reduces Total $CD1^{hi}/IgM^{hi}$ B Cell Populations in Spleens of Baff Tg Mice

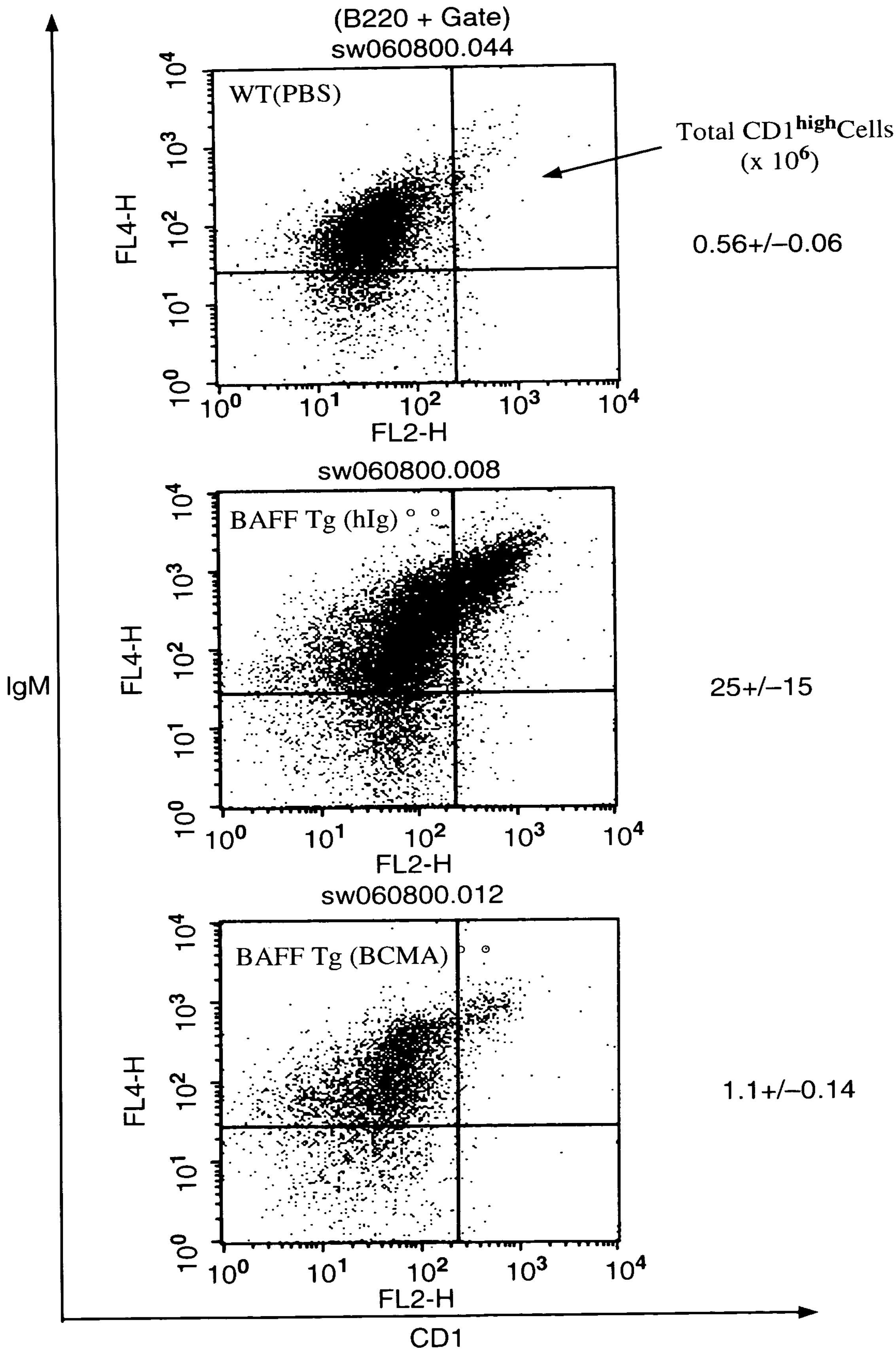


FIG. 10B

BCMA-Ig Treatment Reduces Total Mature B and T2 B Cell Populations in Spleens of Baff Tg Mice

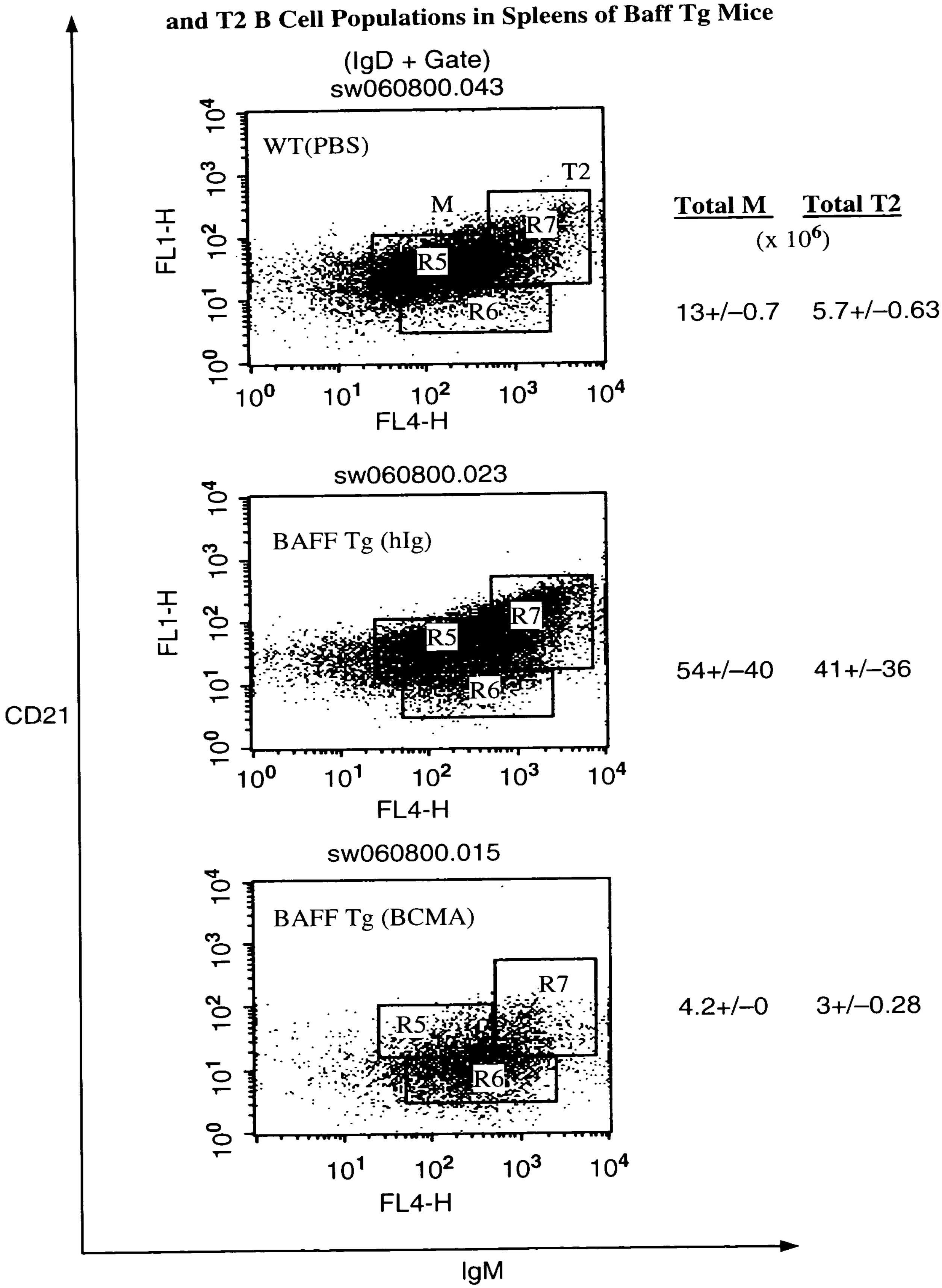
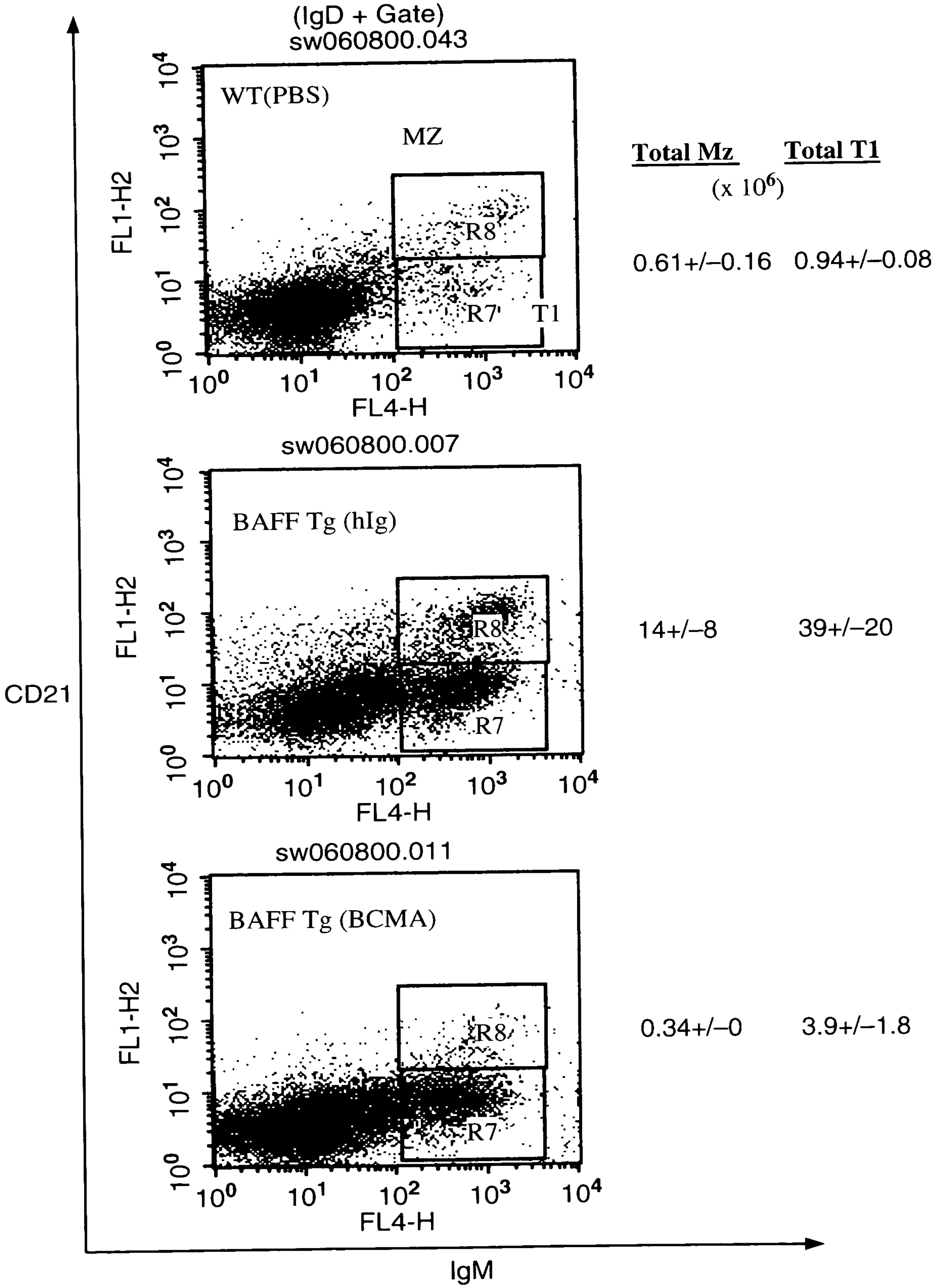


FIG. 10C

BCMA-Ig Treatment Reduces Total Marginal Zone and T1 B Cell Populations in Spleens of Baff Tg Mice



hBCMA-hIg Treatment Reduces Spleen Weight in BAFF Tg Mice

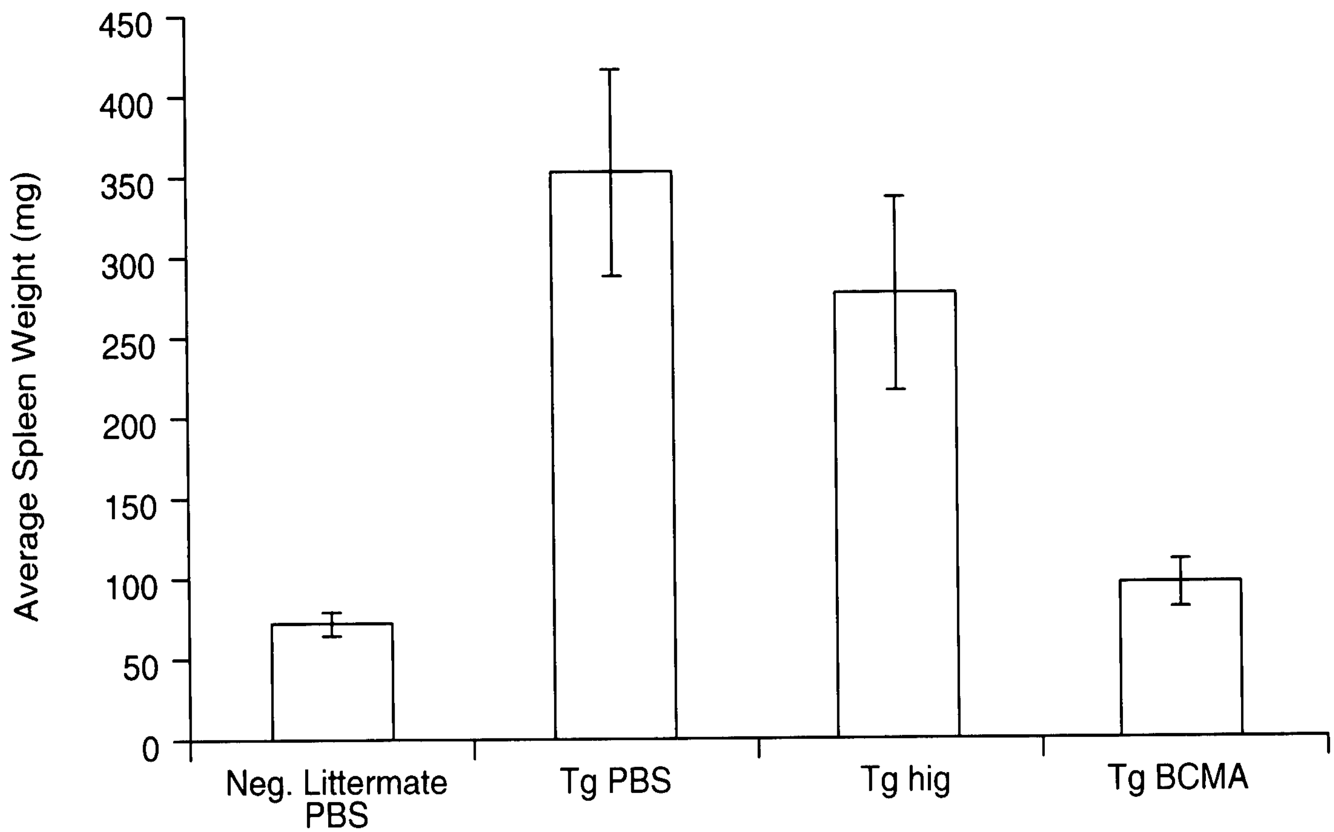


FIG. 11

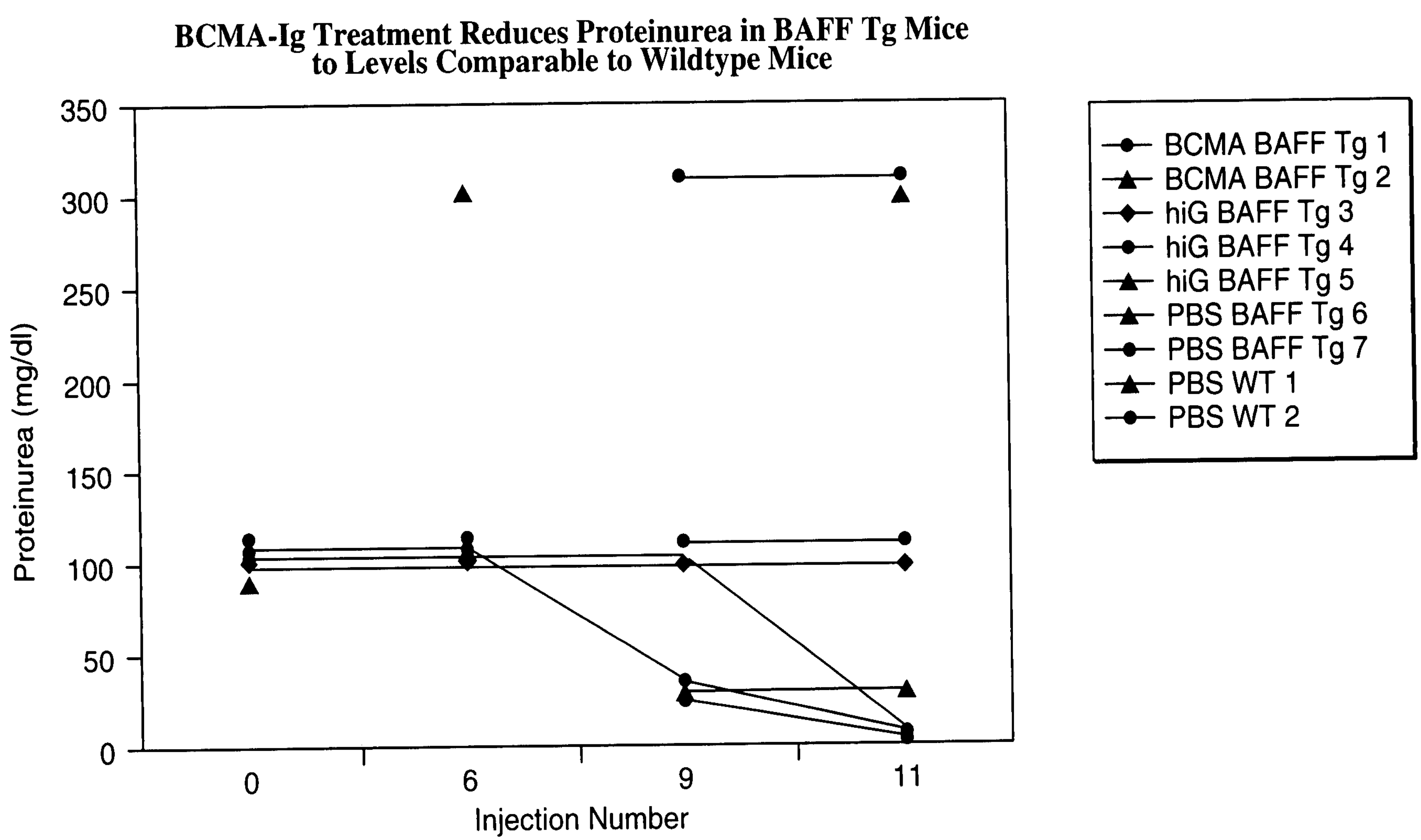

BCMA-Ig Treatment Reduces Proteinurea in BAFF Tg Mice to Levels Comparable to Wildtype Mice
Proteinurea (mg/dl)
350
300
250
200
150
100
50
0
0
6
9
11
Injection Number
BCMA BAFF Tg 1
BCMA BAFF Tg 2
hiG BAFF Tg 3
hiG BAFF Tg 4
hiG BAFF Tg 5
PBS BAFF Tg 6
PBS BAFF Tg 7
PBS WT 1
PBS WT 2

FIG. 12

Average Mean Arterial Pressure in BAFF transgenic (BAFF +) and wild-type controls (BAFF –)

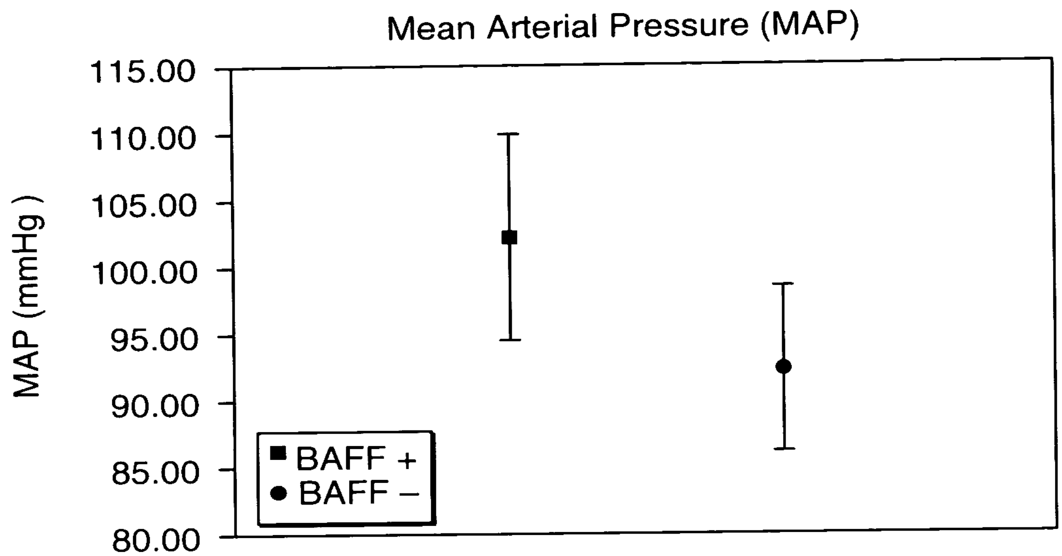


FIG. 13

Individual Mean Arterial Pressure in BAFF transgenic (BAFF +) and wild-type controls (BAFF –)

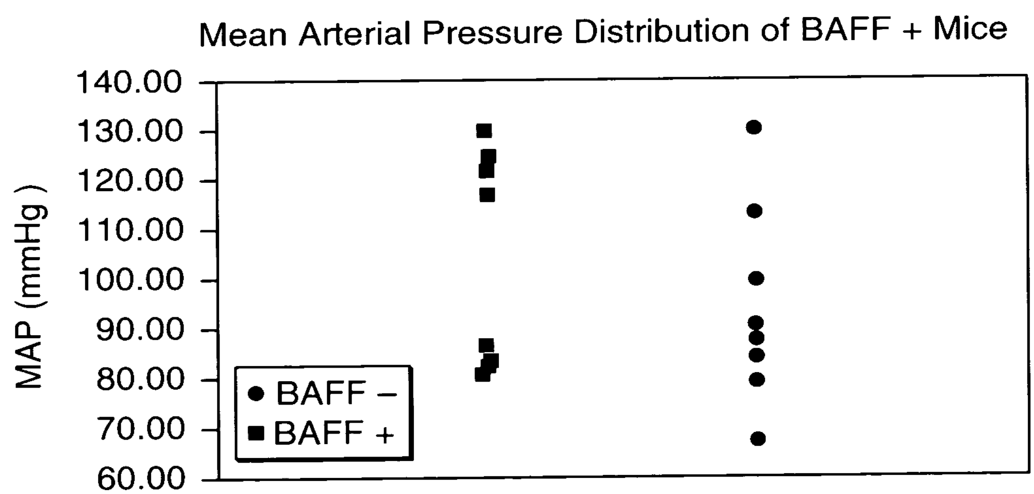


FIG. 14

BCMA-Ig Treatment of Moderately Nephritic SNF1 Mice
Slows Progression to Severe Nephritis

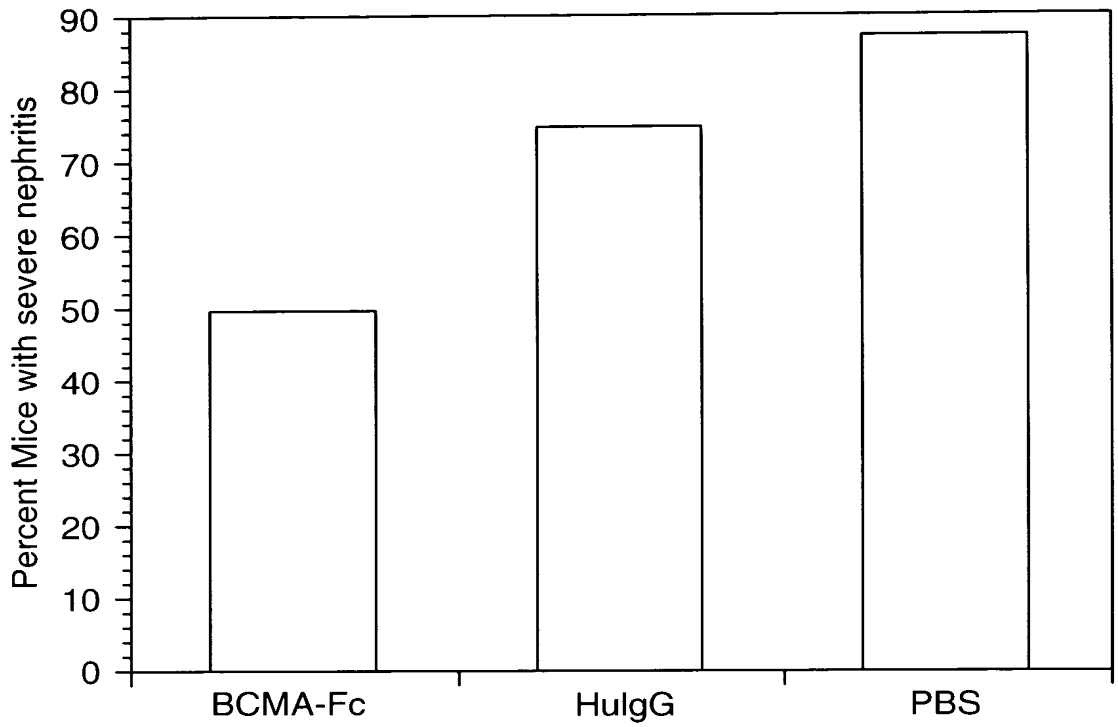


FIG. 15

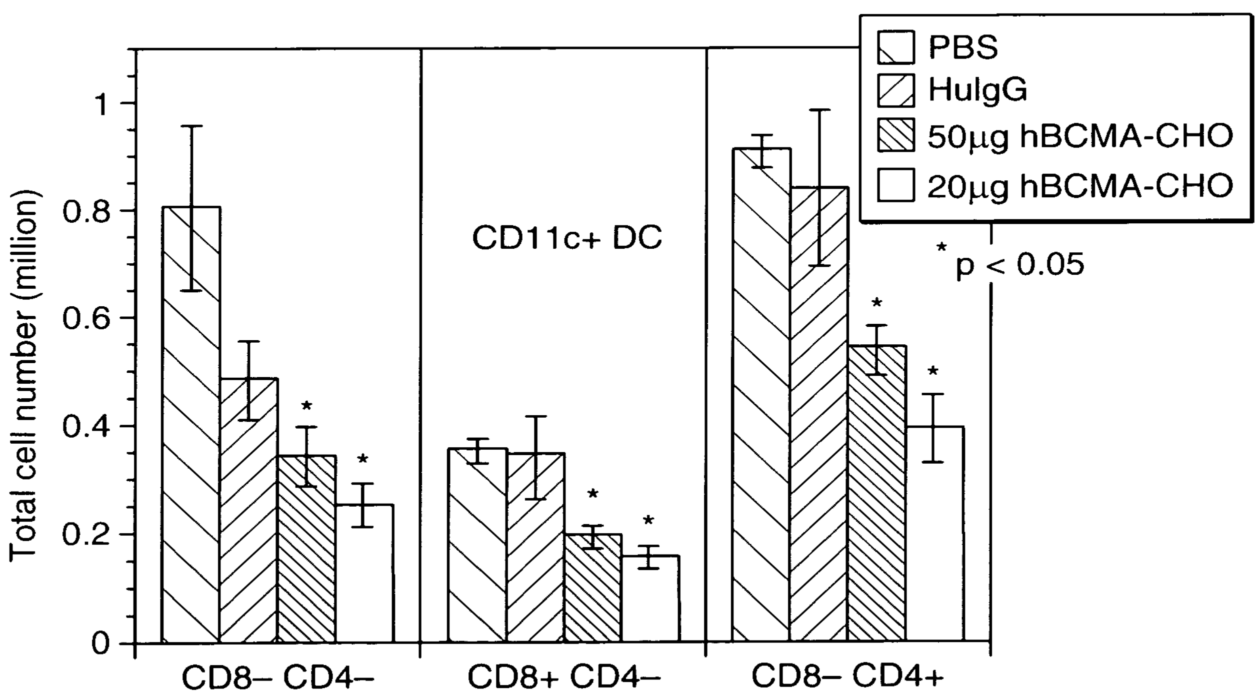


FIG. 16